SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Chambon, Pierre
                 Gronemeyer, Hinrich
                 Voegel, Johannes
                 Lutz, Yves

  (ii) TITLE OF INVENTION: Transcriptional Intermediary Factor-2

(iii) NUMBER OF SEQUENCES: 14

 (iv) CORRESPONDENCE ADDRESS:
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     (D) STATE: DC
     (E) COUNTRY: USA
     (F) ZIP: 20005-3934

  (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Floppy disk
     (B) COMPUTER: IBM PC compatible
     (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

 (vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER: To be assigned
     (B) FILING DATE: Herewith
     (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: US 60/021,247
     (B) FILING DATE: 12-JUL-1996

(viii) ATTORNEY/AGENT INFORMATION:
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     (C) REFERENCE/DOCKET NUMBER: 1383.0130001/EKS

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(2) INFORMATION FOR SEQ ID NO:1:

  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 6156 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
    (A) NAME/KEY: CDS
    (B) LOCATION: 163..4554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGCGGCCGCA GCCTCGGCTA CAGCTTCGGC GGCGAAGGTC AGCGCCGACG GCAGCCGGCA        60

CCTGACGGCG TGACCGACCC GAGCCGATTT CTCTTGGATT TGGCTACACA CTTATAGATC       120

TTCTGCACTG TTTACAGGCA CAGTTGCTGA TATGTGTTCA AG ATG AGT GGG ATG         174
                                              Met Ser Gly Met
                                                1

GGA GAA AAT ACC TCT GAC CCC TCC AGG GCA GAG ACA AGA AAG CGC AAG        222
Gly Glu Asn Thr Ser Asp Pro Ser Arg Ala Glu Thr Arg Lys Arg Lys
 5               10               15               20

GAA TGT CCT GAC CAA CTT GGA CCC AGC CCC AAA AGG AAC ACT GAA AAA        270
Glu Cys Pro Asp Gln Leu Gly Pro Ser Pro Lys Arg Asn Thr Glu Lys
             25               30               35

CGT AAT CGT GAA CAG GAA AAT AAA TAT ATA GAA GAA CTT GCA GAG TTG        318
Arg Asn Arg Glu Gln Glu Asn Lys Tyr Ile Glu Glu Leu Ala Glu Leu
         40               45               50

ATT TTT GCA AAT TTT AAT GAT ATA GAC AAC TTT AAC TTC AAA CCT GAC        366
Ile Phe Ala Asn Phe Asn Asp Ile Asp Asn Phe Asn Phe Lys Pro Asp
             55               60               65

AAA TGT GCA ATC TTA AAA GAA ACT GTG AAG CAA ATT CGT CAG ATC AAA        414
Lys Cys Ala Ile Leu Lys Glu Thr Val Lys Gln Ile Arg Gln Ile Lys
         70               75               80

GAA CAA GAG AAA GCA GCA GCT GCC AAC ATA GAT GAA GTG CAG AAG TCA        462
Glu Gln Glu Lys Ala Ala Ala Ala Asn Ile Asp Glu Val Gln Lys Ser
 85               90               95              100

GAT GTA TCC TCT ACA GGG CAG GGT GTC ATC GAC AAG GAT GCG CTG GGG        510
Asp Val Ser Ser Thr Gly Gln Gly Val Ile Asp Lys Asp Ala Leu Gly
             105              110              115

CCT ATG ATG CTT GAG GCC CTT GAT GGG TTC TTC TTT GTA GTG AAC CTG        558
Pro Met Met Leu Glu Ala Leu Asp Gly Phe Phe Phe Val Val Asn Leu
             120              125              130

GAA GGC AAC GTT GTG TTT GTG TCA GAG AAT GTG ACA CAG TAT CTA AGG        606
Glu Gly Asn Val Val Phe Val Ser Glu Asn Val Thr Gln Tyr Leu Arg
             135              140              145

TAT AAC CAA GAA GAG CTG ATG AAC AAA AGT GTA TAT AGC ATC TTG CAT        654
Tyr Asn Gln Glu Glu Leu Met Asn Lys Ser Val Tyr Ser Ile Leu His
 150              155              160

GTT GGG GAC CAC ACG GAA TTT GTC AAA AAC CTG CTG CCA AAG TCT ATA        702
Val Gly Asp His Thr Glu Phe Val Lys Asn Leu Leu Pro Lys Ser Ile
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	165			170			175			180	

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      GTA AAT GGG GGA TCT TGG TCT GGC GAA CCT CCG AGG CGG AAC AGC CAT      750
      Val Asn Gly Gly Ser Trp Ser Gly Glu Pro Pro Arg Arg Asn Ser His
                      185             190             195

      ACC TTC AAT TGT CGG ATG CTG GTA AAA CCT TTA CCT GAT TCA GAA GAG      798
      Thr Phe Asn Cys Arg Met Leu Val Lys Pro Leu Pro Asp Ser Glu Glu
                  200             205             210

      GAG GGT CAT GAT AAC CAG GAA GCT CAT CAG AAA TAT GAA ACT ATG CAG      846
      Glu Gly His Asp Asn Gln Glu Ala His Gln Lys Tyr Glu Thr Met Gln
                  215             220             225

      TGC TTC GCT GTC TCT CAA CCA AAG TCC ATC AAA GAA GAA GGA GAA GAT      894
      Cys Phe Ala Val Ser Gln Pro Lys Ser Ile Lys Glu Glu Gly Glu Asp
                  230             235             240

      TTG CAG TCC TGC TTG ATT TGC GTG GCA AGA AGA GTT CCC ATG AAG GAA      942
      Leu Gln Ser Cys Leu Ile Cys Val Ala Arg Arg Val Pro Met Lys Glu
      245             250             255             260

      AGA CCA GTT CTT CCC TCA TCA GAA AGT TTT ACT ACT CGC CAG GAT CTC      990
      Arg Pro Val Leu Pro Ser Ser Glu Ser Phe Thr Thr Arg Gln Asp Leu
                      265             270             275

      CAA GGC AAG ATC ACG TCT CTG GAT ACC AGC ACC ATG AGA GCA GCC ATG      1038
      Gln Gly Lys Ile Thr Ser Leu Asp Thr Ser Thr Met Arg Ala Ala Met
                      280             285             290

      AAA CCA GGC TGG GAG GAC CTG GTA AGA AGG TGT ATT CAG AAG TTC CAT      1086
      Lys Pro Gly Trp Glu Asp Leu Val Arg Arg Cys Ile Gln Lys Phe His
                      295             300             305

      GCG CAG CAT GAA GGA GAA TCT GTG TCC TAT GCT AAG AGG CAT CAT CAT      1134
      Ala Gln His Glu Gly Glu Ser Val Ser Tyr Ala Lys Arg His His His
          310             315             320

      GAA GTA CTG AGA CAA GGA TTG GCA TTC AGT CAA ATC TAT CGT TTT TCC      1182
      Glu Val Leu Arg Gln Gly Leu Ala Phe Ser Gln Ile Tyr Arg Phe Ser
      325             330             335             340

      TTG TCT GAT GGC ACT CTT GTT GCT GCA CAA ACG AAG AGC AAA CTC ATC      1230
      Leu Ser Asp Gly Thr Leu Val Ala Ala Gln Thr Lys Ser Lys Leu Ile
                      345             350             355

      CGT TCT CAG ACT ACT AAT GAA CCT CAA CTT GTA ATA TCT TTA CAT ATG      1278
      Arg Ser Gln Thr Thr Asn Glu Pro Gln Leu Val Ile Ser Leu His Met
                      360             365             370

      CTT CAC AGA GAG CAG AAT GTG TGT GTG ATG AAT CCG GAT CTG ACT GGA      1326
      Leu His Arg Glu Gln Asn Val Cys Val Met Asn Pro Asp Leu Thr Gly
                  375             380             385

      CAA ACG ATG GGG AAG CCA CTG AAT CCA ATT AGC TCT AAC AGC CCT GCC      1374
      Gln Thr Met Gly Lys Pro Leu Asn Pro Ile Ser Ser Asn Ser Pro Ala
          390             395             400
```

CAT CAG GCC CTG TGC AGT GGG AAC CCA GGT CAG GAC ATG ACC CTC AGT   1422
His Gln Ala Leu Cys Ser Gly Asn Pro Gly Gln Asp Met Thr Leu Ser
405   410   415   420

AGC AAT ATA AAT TTT CCC ATA AAT GGC CCA AAG GAA CAA ATG GGC ATG   1470
Ser Asn Ile Asn Phe Pro Ile Asn Gly Pro Lys Glu Gln Met Gly Met
                  425   430   435

CCC ATG GGC AGG TTT GGT GGT TCT GGG GGA ATG AAC CAT GTG TCA GGC   1518
Pro Met Gly Arg Phe Gly Gly Ser Gly Gly Met Asn His Val Ser Gly
                  440   445   450

ATG CAA GCA ACC ACT CCT CAG GGT AGT AAC TAT GCA CTC AAA ATG AAC   1566
Met Gln Ala Thr Thr Pro Gln Gly Ser Asn Tyr Ala Leu Lys Met Asn
                  455   460   465

AGC CCC TCA CAA AGC AGC CCT GGC ATG AAT CCA GGA CAG CCC ACC TCC   1614
Ser Pro Ser Gln Ser Ser Pro Gly Met Asn Pro Gly Gln Pro Thr Ser
                  470   475   480

ATG CTT TCA CCA AGG CAT CGC ATG AGC CCT GGA GTG GCT GGC AGC CCT   1662
Met Leu Ser Pro Arg His Arg Met Ser Pro Gly Val Ala Gly Ser Pro
485   490   495   500

CGA ATC CCA CCC AGT CAG TTT TCC CCT GCA GGA AGC TTG CAT TCC CCT   1710
Arg Ile Pro Pro Ser Gln Phe Ser Pro Ala Gly Ser Leu His Ser Pro
                  505   510   515

GTG GGA GTT TGC AGC AGC ACA GGA AAT AGC CAT AGT TAT ACC AAC AGC   1758
Val Gly Val Cys Ser Ser Thr Gly Asn Ser His Ser Tyr Thr Asn Ser
                  520   525   530

TCC CTC AAT GCA CTT CAG GCC CTC AGC GAG GGG CAC GGG GTC TCA TTA   1806
Ser Leu Asn Ala Leu Gln Ala Leu Ser Glu Gly His Gly Val Ser Leu
                  535   540   545

GGG TCA TCG TTG GCT TCA CCA GAC CTA AAA ATG GGC AAT TTG CAA AAC   1854
Gly Ser Ser Leu Ala Ser Pro Asp Leu Lys Met Gly Asn Leu Gln Asn
                  550   555   560

TCC CCA GTT AAT ATG AAT CCT CCC CCA CTC AGC AAG ATG GGA AGC TTG   1902
Ser Pro Val Asn Met Asn Pro Pro Pro Leu Ser Lys Met Gly Ser Leu
565   570   575   580

GAC TCA AAA GAC TGT TTT GGA CTA TAT GGG GAG CCC TCT GAA GGT ACA   1950
Asp Ser Lys Asp Cys Phe Gly Leu Tyr Gly Glu Pro Ser Glu Gly Thr
                  585   590   595

ACT GGA CAA GCA GAG AGC AGC TGC CAT CCT GGA GAG CAA AAG GAA ACA   1998
Thr Gly Gln Ala Glu Ser Ser Cys His Pro Gly Glu Gln Lys Glu Thr
                  600   605   610

AAT GAC CCC AAC CTG CCC CCG GCC GTG AGC AGT GAG AGA GCT GAC GGG   2046
Asn Asp Pro Asn Leu Pro Pro Ala Val Ser Ser Glu Arg Ala Asp Gly
                  615   620   625

CAG AGC AGA CTG CAT GAC AGC AAA GGG CAG ACC AAA CTC CTG CAG CTG   2094

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Gln Ser Arg Leu His Asp Ser Lys Gly Gln Thr Lys Leu Leu Gln Leu
    630             635             640
```

```
CTG ACC ACC AAA TCT GAT CAG ATG GAG CCC TCG CCC TTA GCC AGC TCT     2142
Leu Thr Thr Lys Ser Asp Gln Met Glu Pro Ser Pro Leu Ala Ser Ser
645             650             655             660
```

```
TTG TCG GAT ACA AAC AAA GAC TCC ACA GGT AGC TTG CCT GGT TCT GGG     2190
Leu Ser Asp Thr Asn Lys Asp Ser Thr Gly Ser Leu Pro Gly Ser Gly
            665             670             675
```

```
TCT ACA CAT GGA ACC TCG CTC AAG GAG AAG CAT AAA ATT TTG CAC AGA     2238
Ser Thr His Gly Thr Ser Leu Lys Glu Lys His Lys Ile Leu His Arg
            680             685             690
```

```
CTC TTG CAG GAC AGC AGT TCC CCT GTG GAC TTG GCC AAG TTA ACA GCA     2286
Leu Leu Gln Asp Ser Ser Ser Pro Val Asp Leu Ala Lys Leu Thr Ala
            695             700             705
```

```
GAA GCC ACA GGC AAA GAC CTG AGC CAG GAG TCC AGC AGC ACA GCT CCT     2334
Glu Ala Thr Gly Lys Asp Leu Ser Gln Glu Ser Ser Ser Thr Ala Pro
    710             715             720
```

```
GGA TCA GAA GTG ACT ATT AAA CAA GAG CCG GTG AGC CCC AAG AAG AAA     2382
Gly Ser Glu Val Thr Ile Lys Gln Glu Pro Val Ser Pro Lys Lys Lys
725             730             735             740
```

```
GAG AAT GCA CTA CTT CGC TAT TTG CTA GAT AAA GAT GAT ACT AAA GAT     2430
Glu Asn Ala Leu Leu Arg Tyr Leu Leu Asp Lys Asp Asp Thr Lys Asp
            745             750             755
```

```
ATT GGT TTA CCA GAA ATA ACC CCC AAA CTT GAG AGA CTG GAC AGT AAG     2478
Ile Gly Leu Pro Glu Ile Thr Pro Lys Leu Glu Arg Leu Asp Ser Lys
            760             765             770
```

```
ACA GAT CCT GCC AGT AAC ACA AAA TTA ATA GCA ATG AAA ACT GAG AAG     2526
Thr Asp Pro Ala Ser Asn Thr Lys Leu Ile Ala Met Lys Thr Glu Lys
            775             780             785
```

```
GAG GAG ATG AGC TTT GAG CCT GGT GAC CAG CCT GGC AGT GAG CTG GAC     2574
Glu Glu Met Ser Phe Glu Pro Gly Asp Gln Pro Gly Ser Glu Leu Asp
    790             795             800
```

```
AAC TTG GAG GAG ATT TTG GAT GAT TTG CAG AAT AGT CAA TTA CCA CAG     2622
Asn Leu Glu Glu Ile Leu Asp Asp Leu Gln Asn Ser Gln Leu Pro Gln
805             810             815             820
```

```
CTT TTC CCA GAC ACG AGG CCA GGC GCC CCT GCT GGA TCA GTT GAC AAG     2670
Leu Phe Pro Asp Thr Arg Pro Gly Ala Pro Ala Gly Ser Val Asp Lys
            825             830             835
```

```
CAA GCC ATC ATC AAT GAC CTC ATG CAA CTC ACA GCT GAA AAC AGC CCT     2718
Gln Ala Ile Ile Asn Asp Leu Met Gln Leu Thr Ala Glu Asn Ser Pro
            840             845             850
```

```
GTC ACA CCT GTT GGA GCC CAG AAA ACA GCA CTG CGA ATT TCA CAG AGC     2766
Val Thr Pro Val Gly Ala Gln Lys Thr Ala Leu Arg Ile Ser Gln Ser
```

```
                855                    860                    865

      ACT TTT AAT AAC CCA CGA CCA GGG CAA CTG GGC AGG TTA TTG CCA AAC      2814
      Thr Phe Asn Asn Pro Arg Pro Gly Gln Leu Gly Arg Leu Leu Pro Asn
          870             875                 880

      CAG AAT TTA CCA CTT GAC ATC ACA TTG CAA AGC CCA ACT GGT GCT GGA      2862
      Gln Asn Leu Pro Leu Asp Ile Thr Leu Gln Ser Pro Thr Gly Ala Gly
      885                 890                 895                 900

      CCT TTC CCA CCA ATC AGA AAC AGT AGT CCC TAC TCA GTG ATA CCT CAG      2910
      Pro Phe Pro Pro Ile Arg Asn Ser Ser Pro Tyr Ser Val Ile Pro Gln
                      905                 910                 915

      CCA GGA ATG ATG GGT AAT CAA GGG ATG ATA GGA AAC CAA GGA AAT TTA      2958
      Pro Gly Met Met Gly Asn Gln Gly Met Ile Gly Asn Gln Gly Asn Leu
              920                 925                 930

      GGG AAC AGT AGC ACA GGA ATG ATT GGT AAC AGT GCT TCT CGG CCT ACT      3006
      Gly Asn Ser Ser Thr Gly Met Ile Gly Asn Ser Ala Ser Arg Pro Thr
              935                 940                 945

      ATG CCA TCT GGA GAA TGG GCA CCG CAG AGT TCG GCT GTG AGA GTC ACC      3054
      Met Pro Ser Gly Glu Trp Ala Pro Gln Ser Ser Ala Val Arg Val Thr
          950                 955                 960

      TGT GCT GCT ACC ACC AGT GCC ATG AAC CGG CCA GTC CAA GGA GGT ATG      3102
      Cys Ala Ala Thr Thr Ser Ala Met Asn Arg Pro Val Gln Gly Gly Met
      965                 970                 975                 980

      ATT CGG AAC CCA GCA GCC AGC ATC CCC ATG AGG CCC AGC AGC CAG CCT      3150
      Ile Arg Asn Pro Ala Ala Ser Ile Pro Met Arg Pro Ser Ser Gln Pro
                      985                 990                 995

      GGC CAA AGA CAG ACG CTT CAG TCT CAG GTC ATG AAT ATA GGG CCA TCT      3198
      Gly Gln Arg Gln Thr Leu Gln Ser Gln Val Met Asn Ile Gly Pro Ser
              1000                1005                1010

      GAA TTA GAG ATG AAC ATG GGG GGA CCT CAG TAT AGC CAA CAA CAA GCT      3246
      Glu Leu Glu Met Asn Met Gly Gly Pro Gln Tyr Ser Gln Gln Gln Ala
              1015                1020                1025

      CCT CCA AAT CAG ACT GCC CCA TGG CCT GAA AGC ATC CTG CCT ATA GAC      3294
      Pro Pro Asn Gln Thr Ala Pro Trp Pro Glu Ser Ile Leu Pro Ile Asp
          1030                1035                1040

      CAG GCG TCT TTT GCC AGC CAA AAC AGG CAG CCA TTT GGC AGT TCT CCA      3342
      Gln Ala Ser Phe Ala Ser Gln Asn Arg Gln Pro Phe Gly Ser Ser Pro
      1045                1050                1055                1060

      GAT GAC TTG CTA TGT CCA CAT CCT GCA GCT GAG TCT CCG AGT GAT GAG      3390
      Asp Asp Leu Leu Cys Pro His Pro Ala Ala Glu Ser Pro Ser Asp Glu
                      1065                1070                1075

      GGA GCT CTC CTG GAC CAG CTG TAT CTG GCC TTG CGG AAT TTT GAT GGC      3438
      Gly Ala Leu Leu Asp Gln Leu Tyr Leu Ala Leu Arg Asn Phe Asp Gly
                      1080                1085                1090
```

```
CTG GAG GAG ATT GAT AGA GCC TTA GGA ATA CCC GAA CTG GTC AGC CAG      3486
Leu Glu Glu Ile Asp Arg Ala Leu Gly Ile Pro Glu Leu Val Ser Gln
        1095                1100                1105

AGC CAA GCA GTA GAT CCA GAA CAG TTC TCA AGT CAG GAT TCC AAC ATC      3534
Ser Gln Ala Val Asp Pro Glu Gln Phe Ser Ser Gln Asp Ser Asn Ile
        1110                1115                1120

ATG CTG GAG CAG AAG GCG CCC GTT TTC CCA CAG CAG TAT GCA TCT CAG      3582
Met Leu Glu Gln Lys Ala Pro Val Phe Pro Gln Gln Tyr Ala Ser Gln
1125                1130                1135                1140

GCA CAA ATG GCC CAG GGT AGC TAT TCT CCC ATG CAA GAT CCA AAC TTT      3630
Ala Gln Met Ala Gln Gly Ser Tyr Ser Pro Met Gln Asp Pro Asn Phe
                1145                1150                1155

CAC ACC ATG GGA CAG CGG CCT AGT TAT GCC ACA CTC CGT ATG CAG CCC      3678
His Thr Met Gly Gln Arg Pro Ser Tyr Ala Thr Leu Arg Met Gln Pro
                1160                1165                1170

AGA CCG GGC CTC AGG CCC ACG GGC CTA GTG CAG AAC CAG CCA AAT CAA      3726
Arg Pro Gly Leu Arg Pro Thr Gly Leu Val Gln Asn Gln Pro Asn Gln
            1175                1180                1185

CTA AGA CTT CAA CTT CAG CAT CGC CTC CAA GCA CAG CAG AAT CGC CAG      3774
Leu Arg Leu Gln Leu Gln His Arg Leu Gln Ala Gln Gln Asn Arg Gln
        1190                1195                1200

CCA CTT ATG AAT CAA ATC AGC AAT GTT TCC AAT GTG AAC TTG ACT CTG      3822
Pro Leu Met Asn Gln Ile Ser Asn Val Ser Asn Val Asn Leu Thr Leu
1205                1210                1215                1220

AGG CCT GGA GTA CCA ACA CAG GCA CCT ATT AAT GCA CAG ATG CTG GCC      3870
Arg Pro Gly Val Pro Thr Gln Ala Pro Ile Asn Ala Gln Met Leu Ala
                1225                1230                1235

CAG AGA CAG AGG GAA ATC CTG AAC CAG CAT CTT CGA CAG AGA CAA ATG      3918
Gln Arg Gln Arg Glu Ile Leu Asn Gln His Leu Arg Gln Arg Gln Met
            1240                1245                1250

CAT CAG CAA CAG CAA GTT CAG CAA CGA ACT TTG ATG ATG AGA GGA CAA      3966
His Gln Gln Gln Gln Val Gln Gln Arg Thr Leu Met Met Arg Gly Gln
            1255                1260                1265

GGG TTG AAT ATG ACA CCA AGC ATG GTG GCT CCT AGT GGT ATG CCA GCA      4014
Gly Leu Asn Met Thr Pro Ser Met Val Ala Pro Ser Gly Met Pro Ala
1270                1275                1280

ACT ATG AGC AAC CCT CGG ATT CCC CAG GCA AAT GCA CAG CAG TTT CCA      4062
Thr Met Ser Asn Pro Arg Ile Pro Gln Ala Asn Ala Gln Gln Phe Pro
1285                1290                1295                1300

TTT CCT CCA AAC TAC GGA ATA AGT CAG CAA CCT GAT CCA GGC TTT ACT      4110
Phe Pro Pro Asn Tyr Gly Ile Ser Gln Gln Pro Asp Pro Gly Phe Thr
                1305                1310                1315

GGG GCT ACG ACT CCC CAG AGC CCA CTT ATG TCA CCC CGA ATG GCA CAT      4158
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    Gly Ala Thr Thr Pro Gln Ser Pro Leu Met Ser Pro Arg Met Ala His
                1320             1325             1330

    ACA CAG AGT CCC ATG ATG CAA CAG TCT CAG GCC AAC CCA GCC TAT CAG      4206
    Thr Gln Ser Pro Met Met Gln Gln Ser Gln Ala Asn Pro Ala Tyr Gln
            1335             1340             1345

    GCC CCC TCC GAC ATA AAT GGA TGG GCG CAG GGG AAC ATG GGC GGA AAC      4254
    Ala Pro Ser Asp Ile Asn Gly Trp Ala Gln Gly Asn Met Gly Gly Asn
            1350             1355             1360

    AGC ATG TTT TCC CAG CAG TCC CCA CCA CAC TTT GGG CAG CAA GCA AAC      4302
    Ser Met Phe Ser Gln Gln Ser Pro Pro His Phe Gly Gln Gln Ala Asn
    1365             1370             1375             1380

    ACC AGC ATG TAC AGT AAC AAC ATG AAC ATC AAT GTG TCC ATG GCG ACC      4350
    Thr Ser Met Tyr Ser Asn Asn Met Asn Ile Asn Val Ser Met Ala Thr
                1385             1390             1395

    AAC ACA GGT GGC ATG AGC AGC ATG AAC CAG ATG ACA GGA CAG ATC AGC      4398
    Asn Thr Gly Gly Met Ser Ser Met Asn Gln Met Thr Gly Gln Ile Ser
                1400             1405             1410

    ATG ACC TCA GTG ACC TCC GTG TCT ACG TCA GGG CTG TCC TCC ATG GGT      4446
    Met Thr Ser Val Thr Ser Val Ser Thr Ser Gly Leu Ser Ser Met Gly
                1415             1420             1425

    CCC GAG CAG GTT AAT GAT CCT GCT CTG AGG GGA GGC AAC CTG TTC CCA      4494
    Pro Glu Gln Val Asn Asp Pro Ala Leu Arg Gly Gly Asn Leu Phe Pro
            1430             1435             1440

    AAC CAG CTG CCT GGA ATG GAT ATG ATT AAG CAG GAG GGA GAC ACA ACA      4542
    Asn Gln Leu Pro Gly Met Asp Met Ile Lys Gln Glu Gly Asp Thr Thr
    1445             1450             1455             1460

    CGG AAA TAT TGC TGACACTGCT GAAGCCAGTT GCTTCTTCAG CTGACCGGGC          4594
    Arg Lys Tyr Cys


    TCACTTGCTC AAAACACTTC CAGTCTGGAG AGCTGTGTCT ATTTGTTTCA ACCCAACTGA    4654

    CCTGCCAGCC GGTTCTGCTA GAGCAGACAG GCCTGGCCCT GGTTCCCAGG GTGGCGTCCA    4714

    CTCGGCTGTG GCAGGAGGAG CTGCCTCTTC TCTTGACAGT CTGAAGCTCG CATCCAGACA    4774

    GTCGCTCAGT CTGTTCCCTG CATTCACCTT AGTGCAACTT AGATCTCTCC TCCCCAAGTA    4834

    AATGTTGACA GGCCAATTTC ATACCCATGT CAGATTGAAT GTATTTAAAT GTATGTATTT    4894

    AAGGAGAACC ATGCTCTTGT TCTGTTCCTG TTCGGTTCCA GACACTGGTT TCTTGCTTTG    4954

    TTTTCCCTGG CTAACAGTCT AGTGCCAAAG ATTAAGATTT TATCTGGGGG AAAGAAAAGA    5014

    ATTTTTTAAA AAATTAAACT AAAGATGTTT TAAGCTAAAG CCTGAATTTG GGATGGAAGC    5074

    AGGACAGACA CCGTGGACAG CGCTGTATTT ACAGACACAC CCAGTGCGTG AAGACCAACA    5134
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AAGTCACAGT CGTATCTCTA GAAAGCTCTA AAGACCATGT TGGAAAGAGT CTCCAGTTAC      5194

TGAACAGATG AAAAGGAGCC TGTGAGAGGG CTGTTAACAT TAGCAAATAT TTTTTCCTTG      5254

TTTTTTCTTT GTTAAAACCA AACTGGTTCA CCTGAATCAT GAATTGAGAA GAAATAATTT      5314

TCATTTCTAA ATTAAGTCCC TTTTAGTTTG ATCAGACAGC TTGAATCAGC ATCTCTTCTT      5374

CCCTGTCAGC CTGACTCTTC CCTTCCCCTC TCTCATTCCC CATACTCCCT ATTTTCATTC      5434

CTTTTTTAAA AAATAATATA AGCTACAGAA ACCAGGTAAG CCCTTTATTT CCTTAAATGT      5494

TTTGCCAGCC ACTTACCAAT TGCTAAGTAT TGAATTTCAG AAAAAAAAAA TGCATTTACT      5554

GGCAAGGAGA AGAGCAAAGT TAAGGCTTGA TACCAATCGA GCTAAGGATA CCTGCTTTGG      5614

AAGCATGTTT ATTCTGTTCC CCAGCAACTC TGGCCTCCAA AATGGGAGAA ACGCCAGTGT      5674

GTTTAAATTG ATAGCAGATA TCACGACAGA TTTAACCTCT GCCATGTGTT TTTTATTTTG      5734

TTTTTTAGCA GTGCTGACTA AGCCGAAGTT TTGTAAGGTA CATAAAATCC AATTTATATG      5794

TAAACAAGCA ATAATTTAAG TTGAGAACTT ATGTGTTTTA ATTGTATAAT TTTTGTGAGG      5854

TATACATATT GTGGAATTGA CTCAAAAATG AGGTACTTCA GTATTAAATT AGATATCTTC      5914

ATAGCAATGT CTCCTAAAGG TGTTTTGTAA AGGATATCAA TGCCTTGATT AGACCTAATT      5974

TGTAGACTTA AGACTTTTTA TTTTCTAAAC CTTGTGATTC TGCTTATAAG TCATTTATCT      6034

AATCTATATG ATATGCAGCC GCTGTAGGAA CCAATTCTTG ATTTTTATAT GTTTATATTC      6094

TTTCTTAATG AACCTTAGAA AGACTACATG TTACTAAGCA GGCCACTTTT ATGGTTGTTT      6154

TT                                                                    6156
```

(2) INFORMATION FOR SEQ ID NO:2:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1464 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Ser Gly Met Gly Glu Asn Thr Ser Asp Pro Ser Arg Ala Glu Thr
 1               5                  10                  15

Arg Lys Arg Lys Glu Cys Pro Asp Gln Leu Gly Pro Ser Pro Lys Arg
            20                  25                  30

Asn Thr Glu Lys Arg Asn Arg Glu Gln Glu Asn Lys Tyr Ile Glu Glu
        35                  40                  45
```

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Leu Ala Glu Leu Ile Phe Ala Asn Phe Asn Asp Ile Asp Asn Phe Asn
    50                  55                  60

Phe Lys Pro Asp Lys Cys Ala Ile Leu Lys Glu Thr Val Lys Gln Ile
65                  70                  75                      80

Arg Gln Ile Lys Glu Gln Glu Lys Ala Ala Ala Ala Asn Ile Asp Glu
                85                  90                  95

Val Gln Lys Ser Asp Val Ser Ser Thr Gly Gln Gly Val Ile Asp Lys
                100                 105                 110

Asp Ala Leu Gly Pro Met Met Leu Glu Ala Leu Asp Gly Phe Phe Phe
        115                 120                 125

Val Val Asn Leu Glu Gly Asn Val Val Phe Val Ser Glu Asn Val Thr
    130                 135                 140

Gln Tyr Leu Arg Tyr Asn Gln Glu Glu Leu Met Asn Lys Ser Val Tyr
145                 150                 155                 160

Ser Ile Leu His Val Gly Asp His Thr Glu Phe Val Lys Asn Leu Leu
                165                 170                     175

Pro Lys Ser Ile Val Asn Gly Gly Ser Trp Ser Gly Glu Pro Pro Arg
                180             185                 190

Arg Asn Ser His Thr Phe Asn Cys Arg Met Leu Val Lys Pro Leu Pro
            195                 200                 205

Asp Ser Glu Glu Glu Gly His Asp Asn Gln Glu Ala His Gln Lys Tyr
    210                 215                 220

Glu Thr Met Gln Cys Phe Ala Val Ser Gln Pro Lys Ser Ile Lys Glu
225                 230                 235                 240

Glu Gly Glu Asp Leu Gln Ser Cys Leu Ile Cys Val Ala Arg Arg Val
            245                 250                 255

Pro Met Lys Glu Arg Pro Val Leu Pro Ser Ser Glu Ser Phe Thr Thr
            260                 265                 270

Arg Gln Asp Leu Gln Gly Lys Ile Thr Ser Leu Asp Thr Ser Thr Met
    275                 280                 285

Arg Ala Ala Met Lys Pro Gly Trp Glu Asp Leu Val Arg Arg Cys Ile
    290                 295                 300

Gln Lys Phe His Ala Gln His Glu Gly Glu Ser Val Ser Tyr Ala Lys
305                 310                 315                 320

Arg His His His Glu Val Leu Arg Gln Gly Leu Ala Phe Ser Gln Ile
            325                 330                 335

Tyr Arg Phe Ser Leu Ser Asp Gly Thr Leu Val Ala Ala Gln Thr Lys
        340                 345                 350
```

```
Ser Lys Leu Ile Arg Ser Gln Thr Thr Asn Glu Pro Gln Leu Val Ile
        355             360             365

Ser Leu His Met Leu His Arg Glu Gln Asn Val Cys Val Met Asn Pro
        370             375             380

Asp Leu Thr Gly Gln Thr Met Gly Lys Pro Leu Asn Pro Ile Ser Ser
385             390             395             400

Asn Ser Pro Ala His Gln Ala Leu Cys Ser Gly Asn Pro Gly Gln Asp
                405             410             415

Met Thr Leu Ser Ser Asn Ile Asn Phe Pro Ile Asn Gly Pro Lys Glu
            420             425             430

Gln Met Gly Met Pro Met Gly Arg Phe Gly Gly Ser Gly Gly Met Asn
        435             440             445

His Val Ser Gly Met Gln Ala Thr Thr Pro Gln Gly Ser Asn Tyr Ala
    450             455             460

Leu Lys Met Asn Ser Pro Ser Gln Ser Ser Pro Gly Met Asn Pro Gly
465             470             475             480

Gln Pro Thr Ser Met Leu Ser Pro Arg His Arg Met Ser Pro Gly Val
            485             490             495

Ala Gly Ser Pro Arg Ile Pro Pro Ser Gln Phe Ser Pro Ala Gly Ser
            500             505             510

Leu His Ser Pro Val Gly Val Cys Ser Ser Thr Gly Asn Ser His Ser
        515             520             525

Tyr Thr Asn Ser Ser Leu Asn Ala Leu Gln Ala Leu Ser Glu Gly His
    530             535             540

Gly Val Ser Leu Gly Ser Ser Leu Ala Ser Pro Asp Leu Lys Met Gly
545             550             555             560

Asn Leu Gln Asn Ser Pro Val Asn Met Asn Pro Pro Pro Leu Ser Lys
            565             570             575

Met Gly Ser Leu Asp Ser Lys Asp Cys Phe Gly Leu Tyr Gly Glu Pro
            580             585             590

Ser Glu Gly Thr Thr Gly Gln Ala Glu Ser Ser Cys His Pro Gly Glu
        595             600             605

Gln Lys Glu Thr Asn Asp Pro Asn Leu Pro Pro Ala Val Ser Ser Glu
    610             615             620

Arg Ala Asp Gly Gln Ser Arg Leu His Asp Ser Lys Gly Gln Thr Lys
625             630             635             640

Leu Leu Gln Leu Leu Thr Thr Lys Ser Asp Gln Met Glu Pro Ser Pro
            645             650             655
```

Leu Ala Ser Ser Leu Ser Asp Thr Asn Lys Asp Ser Thr Gly Ser Leu
        660   665   670

Pro Gly Ser Gly Ser Thr His Gly Thr Ser Leu Lys Glu Lys His Lys
        675   680   685

Ile Leu His Arg Leu Leu Gln Asp Ser Ser Ser Pro Val Asp Leu Ala
    690   695   700

Lys Leu Thr Ala Glu Ala Thr Gly Lys Asp Leu Ser Gln Glu Ser Ser
705   710   715   720

Ser Thr Ala Pro Gly Ser Glu Val Thr Ile Lys Gln Glu Pro Val Ser
                725   730   735

Pro Lys Lys Lys Glu Asn Ala Leu Leu Arg Tyr Leu Leu Asp Lys Asp
        740   745   750

Asp Thr Lys Asp Ile Gly Leu Pro Glu Ile Thr Pro Lys Leu Glu Arg
        755   760   765

Leu Asp Ser Lys Thr Asp Pro Ala Ser Asn Thr Lys Leu Ile Ala Met
    770   775   780

Lys Thr Glu Lys Glu Glu Met Ser Phe Glu Pro Gly Asp Gln Pro Gly
785   790   795   800

Ser Glu Leu Asp Asn Leu Glu Glu Ile Leu Asp Asp Leu Gln Asn Ser
                805   810   815

Gln Leu Pro Gln Leu Phe Pro Asp Thr Arg Pro Gly Ala Pro Ala Gly
        820   825   830

Ser Val Asp Lys Gln Ala Ile Ile Asn Asp Leu Met Gln Leu Thr Ala
        835   840   845

Glu Asn Ser Pro Val Thr Pro Val Gly Ala Gln Lys Thr Ala Leu Arg
    850   855   860

Ile Ser Gln Ser Thr Phe Asn Asn Pro Arg Pro Gly Gln Leu Gly Arg
865   870   875   880

Leu Leu Pro Asn Gln Asn Leu Pro Leu Asp Ile Thr Leu Gln Ser Pro
            885   890   895

Thr Gly Ala Gly Pro Phe Pro Pro Ile Arg Asn Ser Ser Pro Tyr Ser
            900   905   910

Val Ile Pro Gln Pro Gly Met Met Gly Asn Gln Gly Met Ile Gly Asn
        915   920   925

Gln Gly Asn Leu Gly Asn Ser Ser Thr Gly Met Ile Gly Asn Ser Ala
    930   935   940

Ser Arg Pro Thr Met Pro Ser Gly Glu Trp Ala Pro Gln Ser Ser Ala
945   950   955   960

```
Val Arg Val Thr Cys Ala Ala Thr Thr Ser Ala Met Asn Arg Pro Val
              965                 970              975

Gln Gly Gly Met Ile Arg Asn Pro Ala Ala Ser Ile Pro Met Arg Pro
          980              985              990

Ser Ser Gln Pro Gly Gln Arg Gln Thr Leu Gln Ser Gln Val Met Asn
          995             1000             1005

Ile Gly Pro Ser Glu Leu Glu Met Asn Met Gly Gly Pro Gln Tyr Ser
   1010             1015             1020

Gln Gln Gln Ala Pro Pro Asn Gln Thr Ala Pro Trp Pro Glu Ser Ile
1025             1030             1035             1040

Leu Pro Ile Asp Gln Ala Ser Phe Ala Ser Gln Asn Arg Gln Pro Phe
             1045             1050             1055

Gly Ser Ser Pro Asp Asp Leu Leu Cys Pro His Pro Ala Ala Glu Ser
          1060             1065             1070

Pro Ser Asp Glu Gly Ala Leu Leu Asp Gln Leu Tyr Leu Ala Leu Arg
          1075             1080             1085

Asn Phe Asp Gly Leu Glu Glu Ile Asp Arg Ala Leu Gly Ile Pro Glu
          1090             1095             1100

Leu Val Ser Gln Ser Gln Ala Val Asp Pro Glu Gln Phe Ser Ser Gln
1105             1110             1115             1120

Asp Ser Asn Ile Met Leu Glu Gln Lys Ala Pro Val Phe Pro Gln Gln
             1125             1130             1135

Tyr Ala Ser Gln Ala Gln Met Ala Gln Gly Ser Tyr Ser Pro Met Gln
          1140             1145             1150

Asp Pro Asn Phe His Thr Met Gly Gln Arg Pro Ser Tyr Ala Thr Leu
   1155             1160             1165

Arg Met Gln Pro Arg Pro Gly Leu Arg Pro Thr Gly Leu Val Gln Asn
   1170             1175             1180

Gln Pro Asn Gln Leu Arg Leu Gln Leu Gln His Arg Leu Gln Ala Gln
1185             1190             1195             1200

Gln Asn Arg Gln Pro Leu Met Asn Gln Ile Ser Asn Val Ser Asn Val
             1205             1210             1215

Asn Leu Thr Leu Arg Pro Gly Val Pro Thr Gln Ala Pro Ile Asn Ala
          1220             1225             1230

Gln Met Leu Ala Gln Arg Gln Arg Glu Ile Leu Asn Gln His Leu Arg
          1235             1240             1245

Gln Arg Gln Met His Gln Gln Gln Val Gln Gln Arg Thr Leu Met
   1250             1255             1260
```

```
Met Arg Gly Gln Gly Leu Asn Met Thr Pro Ser Met Val Ala Pro Ser
1265                1270                1275                1280

Gly Met Pro Ala Thr Met Ser Asn Pro Arg Ile Pro Gln Ala Asn Ala
                1285                1290                1295

Gln Gln Phe Pro Phe Pro Pro Asn Tyr Gly Ile Ser Gln Gln Pro Asp
            1300                1305                1310

Pro Gly Phe Thr Gly Ala Thr Thr Pro Gln Ser Pro Leu Met Ser Pro
            1315                1320                1325

Arg Met Ala His Thr Gln Ser Pro Met Met Gln Gln Ser Gln Ala Asn
    1330                1335                1340

Pro Ala Tyr Gln Ala Pro Ser Asp Ile Asn Gly Trp Ala Gln Gly Asn
1345                1350                1355                1360

Met Gly Gly Asn Ser Met Phe Ser Gln Gln Ser Pro Pro His Phe Gly
                1365                1370                1375

Gln Gln Ala Asn Thr Ser Met Tyr Ser Asn Asn Met Asn Ile Asn Val
            1380                1385                1390

Ser Met Ala Thr Asn Thr Gly Gly Met Ser Ser Met Asn Gln Met Thr
        1395                1400                1405

Gly Gln Ile Ser Met Thr Ser Val Thr Ser Val Ser Thr Ser Gly Leu
        1410                1415                1420

Ser Ser Met Gly Pro Glu Gln Val Asn Asp Pro Ala Leu Arg Gly Gly
1425                1430                1435                1440

Asn Leu Phe Pro Asn Gln Leu Pro Gly Met Asp Met Ile Lys Gln Glu
            1445                1450                1455

Gly Asp Thr Thr Arg Lys Tyr Cys
            1460
```

(2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1036 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: not relevant

        (ii) MOLECULE TYPE: peptide

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Ser Ile Pro Arg Val Asn Pro Ser Val Asn Pro Ser Ile Ser Pro
1                5                10                15
```

Ala His Gly Val Ala Arg Ser Ser Thr Leu Pro Pro Ser Asn Ser Asn
        20   25   30

Met Val Ser Thr Arg Ile Asn Arg Gln Gln Ser Ser Asp Leu His Ser
        35   40   45

Ser Ser His Ser Asn Ser Ser Asn Ser Gln Gly Ser Phe Gly Cys Ser
    50   55   60

Pro Gly Ser Gln Ile Val Ala Asn Val Ala Leu Asn Lys Gly Gln Ala
65   70   75   80

Ser Ser Gln Ser Ser Lys Pro Ser Leu Asn Leu Asn Asn Pro Pro Met
                85   90   95

Glu Gly Thr Gly Ile Ser Leu Ala Gln Phe Met Ser Pro Arg Arg Gln
                100   105   110

Val Thr Ser Gly Leu Ala Thr Arg Pro Arg Met Pro Asn Asn Ser Phe
        115   120   125

Pro Pro Asn Ile Ser Thr Leu Ser Ser Pro Val Gly Met Thr Ser Ser
    130   135   140

Ala Cys Asn Asn Asn Asn Arg Ser Tyr Ser Asn Ile Pro Val Thr Ser
145   150   155   160

Leu Gln Gly Met Asn Glu Gly Pro Asn Asn Ser Val Gly Phe Ser Ala
                165   170   175

Ser Ser Pro Val Leu Arg Gln Met Ser Ser Gln Asn Ser Pro Ser Arg
                180   185   190

Leu Asn Ile Gln Pro Ala Lys Ala Glu Ser Lys Asp Asn Lys Glu Ile
        195   200   205

Ala Ser Thr Leu Asn Glu Met Ile Gln Ser Asp Asn Ser Ser Ser Asp
    210   215   220

Gly Lys Pro Leu Asp Ser Gly Leu Leu His Asn Asn Asp Arg Leu Ser
225   230   235   240

Asp Gly Asp Ser Lys Tyr Ser Gln Thr Ser His Lys Leu Val Gln Leu
                245   250   255

Leu Thr Thr Thr Ala Glu Gln Gln Leu Arg His Ala Asp Ile Asp Thr
                260   265   270

Ser Cys Lys Asp Val Leu Ser Cys Thr Gly Thr Ser Asn Ser Ala Ser
    275   280   285

Ala Asn Ser Ser Gly Gly Ser Cys Pro Ser Ser His Ser Ser Leu Thr
    290   295   300

Ala Arg His Lys Ile Leu His Arg Leu Leu Gln Glu Gly Ser Pro Ser
305   310   315   320

```
Asp Ile Thr Thr Leu Ser Val Glu Pro Asp Lys Lys Asp Ser Ala Ser
              325                 330                 335

Thr Ser Val Ser Val Thr Gly Gln Val Gln Gly Asn Ser Ser Ile Lys
              340                 345                 350

Leu Glu Leu Asp Ala Ser Lys Lys Glu Ser Lys Asp His Gln Leu
              355                 360                 365

Leu Arg Tyr Leu Leu Asp Lys Asp Glu Lys Asp Leu Arg Ser Thr Pro
    370                 375                 380

Asn Leu Ser Leu Asp Asp Val Lys Val Lys Val Glu Lys Lys Glu Gln
385                 390                 395                 400

Met Asp Pro Cys Asn Thr Asn Pro Thr Pro Met Thr Lys Ala Thr Pro
              405                 410                 415

Glu Glu Ile Lys Leu Glu Ala Gln Ser Gln Phe Thr Ala Asp Leu Asp
              420                 425                 430

Gln Phe Asp Gln Leu Leu Pro Thr Leu Glu Lys Ala Ala Gln Leu Pro
    435                 440                 445

Gly Leu Cys Glu Thr Asp Arg Met Asp Gly Ala Val Thr Ser Val Thr
    450                 455                 460

Ile Lys Ser Glu Ile Thr Ile Lys Ser Glu Ile Leu Pro Ala Ser Leu
465                 470                 475                 480

Gln Ser Ala Thr Ala Arg Pro Thr Ser Arg Leu Asn Arg Leu Pro Glu
              485                 490                 495

Leu Glu Leu Glu Ala Ile Asp Asn Gln Phe Gly Gln Pro Gly Thr Gly
              500                 505                 510

Asp Gln Ile Pro Trp Thr Asn Asn Thr Val Thr Ala Ile Asn Gln Ser
    515                 520                 525

Lys Ser Glu Asp Gln Cys Ile Ser Ser Gln Leu Asp Glu Leu Leu Cys
    530                 535                 540

Pro Pro Thr Thr Val Glu Gly Arg Asn Asp Glu Lys Ala Leu Leu Glu
545                 550                 555                 560

Gln Leu Val Ser Phe Leu Ser Gly Lys Asp Glu Thr Glu Leu Ala Glu
              565                 570                 575

Leu Asp Arg Ala Leu Gly Ile Asp Lys Leu Val Gln Gly Gly Gly Leu
              580                 585                 590

Asp Val Leu Ser Glu Arg Phe Pro Pro Gln Gln Ala Thr Pro Pro Leu
              595                 600                 605

Ile Met Glu Glu Arg Pro Asn Leu Tyr Ser Gln Pro Tyr Ser Ser Pro
    610                 615                 620
```

```
Phe Pro Thr Ala Asn Leu Pro Ser Pro Phe Gln Gly Met Val Arg Gln
625             630             635             640

Lys Pro Ser Leu Gly Thr Met Pro Val Gln Val Thr Pro Pro Arg Gly
                645             650             655

Ala Phe Ser Pro Gly Met Gly Met Gln Pro Arg Gln Thr Leu Asn Arg
            660             665             670

Pro Pro Ala Ala Pro Asn Gln Leu Arg Leu Gln Leu Gln Gln Arg Leu
        675             680             685

Gln Gly Gln Gln Gln Leu Ile His Gln Asn Arg Gln Ala Ile Leu Asn
    690             695             700

Gln Phe Ala Ala Thr Ala Pro Val Gly Ile Asn Met Arg Ser Gly Met
705             710             715             720

Gln Gln Gln Ile Thr Pro Gln Pro Pro Leu Asn Ala Gln Met Leu Ala
            725             730             735

Gln Arg Gln Arg Glu Leu Tyr Ser Gln Gln His Arg Gln Arg Gln Leu
        740             745             750

Ile Gln Gln Gln Arg Ala Met Leu Met Arg Gln Gln Ser Phe Gly Asn
    755             760             765

Asn Leu Pro Pro Ser Ser Gly Leu Pro Val Gln Thr Gly Asn Pro Arg
    770             775             780

Leu Pro Gln Gly Ala Pro Gln Gln Phe Pro Tyr Pro Pro Asn Tyr Gly
785             790             795             800

Thr Asn Pro Gly Thr Pro Pro Ala Ser Thr Ser Pro Phe Ser Gln Leu
            805             810             815

Ala Ala Asn Pro Glu Ala Ser Leu Ala Asn Arg Asn Ser Met Val Ser
        820             825             830

Arg Gly Met Thr Gly Asn Ile Gly Gly Gln Phe Gly Thr Gly Ile Asn
    835             840             845

Pro Gln Met Gln Gln Asn Val Phe Gln Tyr Pro Gly Ala Gly Met Val
    850             855             860

Pro Gln Gly Glu Ala Asn Phe Ala Pro Ser Leu Ser Pro Gly Ser Ser
865             870             875             880

Met Val Pro Met Pro Ile Pro Pro Pro Gln Ser Ser Leu Leu Gln Gln
            885             890             895

Thr Pro Pro Ala Ser Gly Tyr Gln Ser Pro Asp Met Lys Ala Trp Gln
        900             905             910

Gln Gly Ala Ile Gly Asn Asn Asn Val Phe Ser Gln Ala Val Gln Asn
    915             920             925
```

```
Gln Pro Thr Pro Ala Gln Pro Gly Val Tyr Asn Asn Met Ser Ile Thr
    930             935             940

Val Ser Met Ala Gly Gly Asn Thr Asn Val Gln Asn Met Asn Pro Met
945             950             955             960

Met Ala Gln Met Gln Met Ser Ser Leu Gln Met Pro Gly Met Asn Thr
            965             970             975

Val Cys Pro Glu Gln Ile Asn Asp Pro Ala Leu Arg His Thr Gly Leu
        980             985             990

Tyr Cys Asn Gln Leu Ser Ser Thr Asp Leu Leu Lys Thr Glu Ala Asp
        995             1000            1005

Gly Thr Gln Gln Val Gln Gln Val Gln Val Phe Ala Asp Val Gln Cys
    1010            1015            1020

Thr Val Asn Leu Val Gly Gly Asp Pro Tyr Leu Asn
1025            1030            1035
```

(2) INFORMATION FOR SEQ ID NO:4:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 21 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: not relevant

  (ii) MOLECULE TYPE: peptide

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Glu Arg Ala Asp Gly Gln Ser Arg Leu His Asp Ser Lys Gly Gln Thr
1               5               10              15

Lys Leu Leu Gln Cys
            20
```

(2) INFORMATION FOR SEQ ID NO:5:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 48 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: not relevant

  (ii) MOLECULE TYPE: peptide

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Gly His Lys Lys Leu Leu Gln Leu Leu Thr Cys Ser Ser His Gly Ser
1               5               10              15
```

```
Leu Leu Gln Glu Lys His Arg Ile Leu His Lys Leu Leu Gln Asn Gly
            20              25              30
```

```
Asn Asn Ala Leu Leu Arg Tyr Leu Leu Asp Arg Asp Asp Pro Ser Asp
            35              40              45
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: not relevant

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Arg Ser Ile Leu Thr Ser Leu Leu Leu Asn Ser Ser
1               5               10
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: not relevant

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Phe Asn Val Leu Lys Gln Leu Leu Leu Ser Glu Asn
1               5               10
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: not relevant

    (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Ala Thr Leu Arg Ser Leu Leu Leu Asn Pro His
1   5   10

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 58 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: not relevant

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Arg Asn Ser Leu Asp Asp Leu Leu Gly Pro Pro Ser Asn Ala Glu
1   5   10   15

Gly Gln Ser Asp Glu Arg Ala Leu Leu Asp Gln Leu His Thr Phe Leu
        20   25   30

Ser Asn Thr Asp Ala Thr Gly Leu Glu Glu Ile Asp Arg Ala Leu Gly
        35   40   45

Ile Pro Glu Leu Val Asn Gln Gly Gln Ala
50   55

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 64 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGACCTGTTG AACTTTGCAA AGGCAAGGGC AGTTCCTTTG AGCTGGGCTT ATGACCTTTG   60

ACTC   64

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 38 base pairs
        (B) TYPE: nucleic acid

            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: cDNA

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGGAGGACAG TCCTCCGGCG GCCGCGGTCA CAGTGACC   38

(2) INFORMATION FOR SEQ ID NO:12:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 5 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: not relevant

      (ii) MOLECULE TYPE: peptide

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Xaa Xaa Leu Leu
1   5

(2) INFORMATION FOR SEQ ID NO:13:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 6 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: not relevant

      (ii) MOLECULE TYPE: peptide

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Xaa Xaa Leu Leu Leu
1   5

(2) INFORMATION FOR SEQ ID NO:14:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 9 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: not relevant

      (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Leu Xaa Xaa Leu Xaa Xaa Xaa Leu
1   5